RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 10/578,085

Source: TAWP

Date Processed by STIC: 1/19/07

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RAW SEQUENCE LISTING   DATE: 01/19/2007
PATENT APPLICATION: **US/10/578,085** TIME: 09:39:07

 Input Set : **A:\50026.058001.txt**
 Output Set: **N:\CRF4\01192007\J578085.raw**

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 3 <110> APPLICANT: Okano, Shinji
 4        Yonemitsu, Yoshikazu
 5        Sueishi, Katsuo
 6        Shibata, Satoko
 7        Hasegawa, Mamoru
 9 <120> TITLE OF INVENTION: Method for Producing Gene Transferred Dendritic Cells
11 <130> FILE REFERENCE: 50026/058001
13 <140> CURRENT APPLICATION NUMBER: US 10/578,085
14 <141> CURRENT FILING DATE: 2006-05-03
16 <150> PRIOR APPLICATION NUMBER: PCT/JP2004/016089
17 <151> PRIOR FILING DATE: 2004-10-29
19 <150> PRIOR APPLICATION NUMBER: JP 2004-187028
20 <151> PRIOR FILING DATE: 2004-06-24
22 <150> PRIOR APPLICATION NUMBER: JP 2003-374808
23 <151> PRIOR FILING DATE: 2003-11-04
25 <160> NUMBER OF SEQ ID NOS: 15
27 <170> SOFTWARE: PatentIn version 3.3
29 <210> SEQ ID NO: 1
30 <211> LENGTH: 10
31 <212> TYPE: DNA
32 <213> ORGANISM: Artificial
34 <220> FEATURE:
35 <223> OTHER INFORMATION: artificially synthesized sequence
37 <400> SEQUENCE: 1
38 ctttcaccct                                                    10
41 <210> SEQ ID NO: 2
42 <211> LENGTH: 15
43 <212> TYPE: DNA
44 <213> ORGANISM: Artificial
46 <220> FEATURE:
47 <223> OTHER INFORMATION: artificially synthesized sequence
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50 tttttcttac tacgg                                              15
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54 <211> LENGTH: 18
55 <212> TYPE: DNA
56 <213> ORGANISM: Artificial
58 <220> FEATURE:
59 <223> OTHER INFORMATION: artificially synthesized sequence
61 <400> SEQUENCE: 3
62 cggccgcaga tcttcacg                                           18
65 <210> SEQ ID NO: 4
66 <211> LENGTH: 18
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 67 <212> TYPE: DNA
 68 <213> ORGANISM: Artificial
 70 <220> FEATURE:
 71 <223> OTHER INFORMATION: artificially synthesized sequence
 73 <400> SEQUENCE: 4
 74 atgcatgccg gcagatga                                            18
 77 <210> SEQ ID NO: 5
 78 <211> LENGTH: 18
 79 <212> TYPE: DNA
 80 <213> ORGANISM: Artificial
 82 <220> FEATURE:
 83 <223> OTHER INFORMATION: artificially synthesized sequence
 85 <400> SEQUENCE: 5
 86 gttgagtact gcaagagc                                            18
 89 <210> SEQ ID NO: 6
 90 <211> LENGTH: 42
 91 <212> TYPE: DNA
 92 <213> ORGANISM: Artificial
 94 <220> FEATURE:
 95 <223> OTHER INFORMATION: artificially synthesized sequence
 97 <400> SEQUENCE: 6
 98 tttgccggca tgcatgtttc ccaaggggag agttttgcaa cc                 42
101 <210> SEQ ID NO: 7
102 <211> LENGTH: 18
103 <212> TYPE: DNA
104 <213> ORGANISM: Artificial
106 <220> FEATURE:
107 <223> OTHER INFORMATION: artificially synthesized sequence
109 <400> SEQUENCE: 7
110 atgcatgccg gcagatga                                            18
113 <210> SEQ ID NO: 8
114 <211> LENGTH: 21
115 <212> TYPE: DNA
116 <213> ORGANISM: Artificial
118 <220> FEATURE:
119 <223> OTHER INFORMATION: artificially synthesized sequence
121 <400> SEQUENCE: 8
122 tgggtgaatg agagaatcag c                                        21
125 <210> SEQ ID NO: 9
126 <211> LENGTH: 10
127 <212> TYPE: PRT
128 <213> ORGANISM: Artificial
130 <220> FEATURE:
131 <223> OTHER INFORMATION: an artificially synthesized peptide
133 <400> SEQUENCE: 9
135 Glu Ala Ala Gly Ile Gly Ile Leu Thr Val
136 1               5                   10
139 <210> SEQ ID NO: 10
140 <211> LENGTH: 10
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141 <212> TYPE: PRT
142 <213> ORGANISM: Artificial
144 <220> FEATURE:
145 <223> OTHER INFORMATION: an artificially synthesized peptide
147 <400> SEQUENCE: 10
149 Glu Leu Ala Gly Ile Gly Ile Leu Thr Val
150 1   5   10
153 <210> SEQ ID NO: 11
154 <211> LENGTH: 9
155 <212> TYPE: PRT
156 <213> ORGANISM: Artificial
158 <220> FEATURE:
159 <223> OTHER INFORMATION: an artificially synthesized peptide
161 <400> SEQUENCE: 11
163 Gly Ile Leu Gly Phe Val Phe Thr Leu
164 1   5
167 <210> SEQ ID NO: 12
168 <211> LENGTH: 561
169 <212> TYPE: DNA
170 <213> ORGANISM: Homo sapiens
173 <220> FEATURE:
174 <221> NAME/KEY: CDS
175 <222> LOCATION: (1)..(561)
177 <220> FEATURE:
178 <221> NAME/KEY: sig_peptide
179 <222> LOCATION: (1)..(21)
181 <400> SEQUENCE: 12
182 atg acc aac aag tgt ctc ctc caa att gct ctc ctg ttg tgc ttc tcc   48
183 Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
184 1   5   10   15
186 act aca gct ctt tcc atg agc tac aac ttg ctt gga ttc cta caa aga   96
187 Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
188   20   25   30
190 agc agc aat ttt cag tgt cag aag ctc ctg tgg caa ttg aat ggg agg   144
191 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
192   35   40   45
194 ctt gaa tat tgc ctc aag gac agg atg aac ttt gac atc cct gag gag   192
195 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
196   50   55   60
198 att aag cag ctg cag cag ttc cag aag gag gac gcc gca ttg acc atc   240
199 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
200 65   70   75   80
202 tat gag atg ctc cag aac atc ttt gct att ttc aga caa gat tca tct   288
203 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
204   85   90   95
206 agc act ggc tgg aat gag act att gtt gag aac ctc ctg gct aat gtc   336
207 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
208   100   105   110
210 tat cat cag ata aac cat ctg aag aca gtc ctg gaa gaa aaa ctg gag   384

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211 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
212         115                 120                 125
214 aaa gaa gat ttt acc agg gga aaa ctc atg agc agt ctg cac ctg aaa        432
215 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
216         130                 135                 140
218 aga tat tat ggg agg att ctg cat tac ctg aag gcc aag gag tac agt        480
219 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
220 145                 150                 155                 160
222 cac tgt gcc tgg acc ata gtc aga gtg gaa atc cta agg aac ttt tac        528
223 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
224                 165                 170                 175
226 ttc att aac aga ctt aca ggt tac ctc cga aac                           561
227 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
228                 180                 185
231 <210> SEQ ID NO: 13
232 <211> LENGTH: 187
233 <212> TYPE: PRT
234 <213> ORGANISM: Homo sapiens
236 <400> SEQUENCE: 13
238 Met Thr Asn Lys Cys Leu Leu Gln Ile Ala Leu Leu Leu Cys Phe Ser
239 1               5                   10                  15
242 Thr Thr Ala Leu Ser Met Ser Tyr Asn Leu Leu Gly Phe Leu Gln Arg
243             20                  25                  30
246 Ser Ser Asn Phe Gln Cys Gln Lys Leu Leu Trp Gln Leu Asn Gly Arg
247         35                  40                  45
250 Leu Glu Tyr Cys Leu Lys Asp Arg Met Asn Phe Asp Ile Pro Glu Glu
251     50                  55                  60
254 Ile Lys Gln Leu Gln Gln Phe Gln Lys Glu Asp Ala Ala Leu Thr Ile
255 65                  70                  75                  80
258 Tyr Glu Met Leu Gln Asn Ile Phe Ala Ile Phe Arg Gln Asp Ser Ser
259                 85                  90                  95
262 Ser Thr Gly Trp Asn Glu Thr Ile Val Glu Asn Leu Leu Ala Asn Val
263             100                 105                 110
266 Tyr His Gln Ile Asn His Leu Lys Thr Val Leu Glu Glu Lys Leu Glu
267         115                 120                 125
270 Lys Glu Asp Phe Thr Arg Gly Lys Leu Met Ser Ser Leu His Leu Lys
271     130                 135                 140
274 Arg Tyr Tyr Gly Arg Ile Leu His Tyr Leu Lys Ala Lys Glu Tyr Ser
275 145                 150                 155                 160
278 His Cys Ala Trp Thr Ile Val Arg Val Glu Ile Leu Arg Asn Phe Tyr
279             165                 170                 175
282 Phe Ile Asn Arg Leu Thr Gly Tyr Leu Arg Asn
283             180                 185
286 <210> SEQ ID NO: 14
287 <211> LENGTH: 546
288 <212> TYPE: DNA
289 <213> ORGANISM: Mus musculus
292 <220> FEATURE:
293 <221> NAME/KEY: CDS
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294 <222> LOCATION: (1)..(546)
296 <220> FEATURE:
297 <221> NAME/KEY: sig_peptide
298 <222> LOCATION: (1)..(21)
300 <400> SEQUENCE: 14
301 atg aac aac agg tgg atc ctc cac gct gcg ttc ctg ctg tgc ttc tcc          48
302 Met Asn Asn Arg Trp Ile Leu His Ala Ala Phe Leu Leu Cys Phe Ser
303 1               5                   10                  15
305 acc aca gcc ctc tcc atc aac tat aag cag ctc cag ctc caa gaa agg          96
306 Thr Thr Ala Leu Ser Ile Asn Tyr Lys Gln Leu Gln Leu Gln Glu Arg
307             20                  25                  30
309 acg aac att cgg aaa tgt cag gag ctc ctg gag cag ctg aat gga aag         144
310 Thr Asn Ile Arg Lys Cys Gln Glu Leu Leu Glu Gln Leu Asn Gly Lys
311          35                  40                  45
313 atc aac ctc acc tac agg gcg gac ttc aag atc cct atg gag atg acg         192
314 Ile Asn Leu Thr Tyr Arg Ala Asp Phe Lys Ile Pro Met Glu Met Thr
315    50                  55                  60
317 gag aag atg cag aag agt tac act gcc ttt gcc atc caa gag atg ctc         240
318 Glu Lys Met Gln Lys Ser Tyr Thr Ala Phe Ala Ile Gln Glu Met Leu
319 65                  70                  75                  80
321 cag aat gtc ttt ctt gtc ttc aga aac aat ttc tcc agc act ggg tgg         288
322 Gln Asn Val Phe Leu Val Phe Arg Asn Asn Phe Ser Ser Thr Gly Trp
323                 85                  90                  95
325 aat gag act att gtt gta cgt ctc ctg gat gaa ctc cac cag cag aca         336
326 Asn Glu Thr Ile Val Val Arg Leu Leu Asp Glu Leu His Gln Gln Thr
327             100                 105                 110
329 gtg ttt ctg aag aca gta cta gag gaa aag caa gag gaa aga ttg acg         384
330 Val Phe Leu Lys Thr Val Leu Glu Glu Lys Gln Glu Glu Arg Leu Thr
331          115                 120                 125
333 tgg gag atg tcc tca act gct ctc cac ttg aag agc tat tac tgg agg         432
334 Trp Glu Met Ser Ser Thr Ala Leu His Leu Lys Ser Tyr Tyr Trp Arg
335       130                 135                 140
337 gtg caa agg tac ctt aaa ctc atg aag tac aac agc tac gcc tgg atg         480
338 Val Gln Arg Tyr Leu Lys Leu Met Lys Tyr Asn Ser Tyr Ala Trp Met
339 145                 150                 155                 160
341 gtg gtc cga gca gag atc ttc agg aac ttt ctc atc att cga aga ctt         528
342 Val Val Arg Ala Glu Ile Phe Arg Asn Phe Leu Ile Ile Arg Arg Leu
343             165                 170                 175
345 acc aga aac ttc caa aac                                                  546
346 Thr Arg Asn Phe Gln Asn
347             180
350 <210> SEQ ID NO: 15
351 <211> LENGTH: 182
352 <212> TYPE: PRT
353 <213> ORGANISM: Mus musculus
355 <400> SEQUENCE: 15
357 Met Asn Asn Arg Trp Ile Leu His Ala Ala Phe Leu Leu Cys Phe Ser
358 1               5                   10                  15
361 Thr Thr Ala Leu Ser Ile Asn Tyr Lys Gln Leu Gln Leu Gln Glu Arg
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RAW SEQUENCE LISTING ERROR SUMMARY   DATE: 01/19/2007
PATENT APPLICATION: **US/10/578,085**   TIME: 09:39:08

Input Set : **A:\50026.058001.txt**
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Invalid <213> Response:
Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:1,2,3,4,5,6,7,8,9,10,11

VERIFICATION SUMMARY   DATE: 01/19/2007
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Input Set : A:\50026.058001.txt
Output Set: N:\CRF4\01192007\J578085.raw